

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Bard, Jonathan A.
Walker, Mary
Branchek, Theresa
Weinshank, Richard L.
- (ii) TITLE OF INVENTION: METHOD OF OBTAINING COMPOSITIONS COMPRISING Y4
SPECIFIC COMPOUNDS
- (iii) NUMBER OF SEQUENCES: 36
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Cooper & Dunham
 - (B) STREET: 1185 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.24
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: White, John P.
 - (B) REGISTRATION NUMBER: 28,678
 - (C) REFERENCE/DOCKET NUMBER: 44743-AA-PCT-US/JPW/JHB
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 278-0400
 - (B) TELEFAX: (212) 391-0525

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 88..1212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGTATTGTTT GTCTGTTTGC CTTGTAGGGC GTCATCCCTC AAGTGTATCA CTTAGTTCAA	60
GAGTCCTGGA ATCTTTTTCAC ATCCACT ATG AAC ACC TCT CAC CTC CTG GCC	111
Met Asn Thr Ser His Leu Leu Ala	
1 5	
TTG CTG CTC CCA AAA TCT CCA CAA GGT GAA AAC AGA AGC AAA CCC CTG	159
Leu Leu Leu Pro Lys Ser Pro Gln Gly Glu Asn Arg Ser Lys Pro Leu	
10 15 20	
GGC ACC CCA TAC AAC TTC TCT GAA CAT TGC CAG GAT TCC GTG GAC GTG	207
Gly Thr Pro Tyr Asn Phe Ser Glu His Cys Gln Asp Ser Val Asp Val	
25 30 35 40	
ATG GTC TTC ATC GTC ACT TCC TAC AGC ATT GAG ACT GTC GTG GGG GTC	255
Met Val Phe Ile Val Thr Ser Tyr Ser Ile Glu Thr Val Val Gly Val	
45 50 55	
CTG GGT AAC CTC TGC CTG ATG TGT GTG ACT GTG AGG CAG AAG GAG AAA	303
Leu Gly Asn Leu Cys Leu Met Cys Val Thr Val Arg Gln Lys Glu Lys	
60 65 70	
GCC AAC GTG ACC AAC CTG CTT ATC GCC AAC CTG GCC TTC TCT GAC TTC	351
Ala Asn Val Thr Asn Leu Leu Ile Ala Asn Leu Ala Phe Ser Asp Phe	
75 80 85	
CTC ATG TGC CTC CTC TGC CAG CCG CTG ACC GCC GTC TAC ACC ATC ATG	399
Leu Met Cys Leu Leu Cys Gln Pro Leu Thr Ala Val Tyr Thr Ile Met	
90 95 100	
GAC TAC TGG ATC TTT GGA GAG ACC CTC TGC AAG ATG TCG GCC TTC ATC	447
Asp Tyr Trp Ile Phe Gly Glu Thr Leu Cys Lys Met Ser Ala Phe Ile	
105 110 115 120	
CAG TGC ATG TCG GTG ACG GTC TCC ATC CTC TCG CTC GTC CTC GTG GCC	495
Gln Cys Met Ser Val Thr Val Ser Ile Leu Ser Leu Val Leu Val Ala	
125 130 135	
CTG GAG AGG CAT CAG CTC ATC ATC AAC CCA ACA GGC TGG AAG CCC AGC	543
Leu Glu Arg His Gln Leu Ile Ile Asn Pro Thr Gly Trp Lys Pro Ser	
140 145 150	
ATC TCA CAG GCC TAC CTG GGG ATT GTG CTC ATC TGG GTC ATT GCC TGT	591
Ile Ser Gln Ala Tyr Leu Gly Ile Val Leu Ile Trp Val Ile Ala Cys	
155 160 165	
GTC CTC TCC CTG CCC TTC CTG GCC AAC AGC ATC CTG GAG AAT GTC TTC	639
Val Leu Ser Leu Pro Phe Leu Ala Asn Ser Ile Leu Glu Asn Val Phe	
170 175 180	
CAC AAG AAC CAC TCC AAG GCT CTG GAG TTC CTG GCA GAT AAG GTG GTC	687
His Lys Asn His Ser Lys Ala Leu Glu Phe Leu Ala Asp Lys Val Val	
185 190 195 200	
TGT ACC GAG TCC TGG CCA CTG GCT CAC CAC CGC ACC ATC TAC ACC ACC	735
Cys Thr Glu Ser Trp Pro Leu Ala His His Arg Thr Ile Tyr Thr Thr	
205 210 215	
TTC CTG CTC CTC TTC CAG TAC TGC CTC CCA CTG GGC TTC ATC CTG GTC	783
Phe Leu Leu Leu Phe Gln Tyr Cys Leu Pro Leu Gly Phe Ile Leu Val	
220 225 230	

TGT TAT GCA CGC ATC TAC CGG CGC CTG CAG AGG CAG GGG CGC GTG TTT	831
Cys Tyr Ala Arg Ile Tyr Arg Arg Leu Gln Arg Gln Gly Arg Val Phe	
235 240 245	
CAC AAG GGC ACC TAC AGC TTG CGA GCT GGG CAC ATG AAG CAG GTC AAT	879
His Lys Gly Thr Tyr Ser Leu Arg Ala Gly His Met Lys Gln Val Asn	
250 255 260	
GTG GTG CTG GTG GTG ATG GTG GTG GCC TTT GCC GTG CTC TGG CTG CCT	927
Val Val Leu Val Val Met Val Val Ala Phe Ala Val Leu Trp Leu Pro	
265 270 275 280	
CTG CAT GTG TTC AAC AGC CTG GAA GAC TGG CAC CAT GAG GCC ATC CCC	975
Leu His Val Phe Asn Ser Leu Glu Asp Trp His His Glu Ala Ile Pro	
285 290 295	
ATC TGC CAC GGG AAC CTC ATC TTC TTA GTG TGC CAC TTG CTT GCC ATG	1023
Ile Cys His Gly Asn Leu Ile Phe Leu Val Cys His Leu Leu Ala Met	
300 305 310	
GCC TCC ACC TGC GTC AAC CCA TTC ATC TAT GGC TTT CTC AAC ACC AAC	1071
Ala Ser Thr Cys Val Asn Pro Phe Ile Tyr Gly Phe Leu Asn Thr Asn	
315 320 325	
TTC AAG AAG GAG ATC AAG GCC CTG GTG CTG ACT TGC CAG CAG AGC GCC	1119
Phe Lys Lys Glu Ile Lys Ala Leu Val Leu Thr Cys Gln Gln Ser Ala	
330 335 340	
CCC CTG GAG GAG TCG GAG CAT CTG CCC CTG TCC ACA GTA CAT ACG GAA	1167
Pro Leu Glu Glu Ser Glu His Leu Pro Leu Ser Thr Val His Thr Glu	
345 350 355 360	
GTC TCC AAA GGG TCC CTG AGG CTA AGT GGC AGG TCC AAT CCC ATT	1212
Val Ser Lys Gly Ser Leu Arg Leu Ser Gly Arg Ser Asn Pro Ile	
365 370 375	
TAACCAGGTC TAGGTCTTCT CCCTGCCATG TCCCTTGCCA GGCTCTTCCA CTTAGCTAAG	1272
TGGGCACACT GCAAGCTGGG GTGGCACCCC AGCATTCCTG GCTTTCTG	1320

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asn Thr Ser His Leu Leu Ala Leu Leu Leu Pro Lys Ser Pro Gln	
1 5 10 15	
Gly Glu Asn Arg Ser Lys Pro Leu Gly Thr Pro Tyr Asn Phe Ser Glu	
20 25 30	
His Cys Gln Asp Ser Val Asp Val Met Val Phe Ile Val Thr Ser Tyr	
35 40 45	
Ser Ile Glu Thr Val Val Gly Val Leu Gly Asn Leu Cys Leu Met Cys	
50 55 60	

Val	Thr	Val	Arg	Gln	Lys	Glu	Lys	Ala	Asn	Val	Thr	Asn	Leu	Leu	Ile	65	70	75	80
Ala	Asn	Leu	Ala	Phe	Ser	Asp	Phe	Leu	Met	Cys	Leu	Leu	Cys	Gln	Pro	85	90	95	
Leu	Thr	Ala	Val	Tyr	Thr	Ile	Met	Asp	Tyr	Trp	Ile	Phe	Gly	Glu	Thr	100	105	110	
Leu	Cys	Lys	Met	Ser	Ala	Phe	Ile	Gln	Cys	Met	Ser	Val	Thr	Val	Ser	115	120	125	
Ile	Leu	Ser	Leu	Val	Leu	Val	Ala	Leu	Glu	Arg	His	Gln	Leu	Ile	Ile	130	135	140	
Asn	Pro	Thr	Gly	Trp	Lys	Pro	Ser	Ile	Ser	Gln	Ala	Tyr	Leu	Gly	Ile	145	150	155	160
Val	Leu	Ile	Trp	Val	Ile	Ala	Cys	Val	Leu	Ser	Leu	Pro	Phe	Leu	Ala	165	170	175	
Asn	Ser	Ile	Leu	Glu	Asn	Val	Phe	His	Lys	Asn	His	Ser	Lys	Ala	Leu	180	185	190	
Glu	Phe	Leu	Ala	Asp	Lys	Val	Val	Cys	Thr	Glu	Ser	Trp	Pro	Leu	Ala	195	200	205	
His	His	Arg	Thr	Ile	Tyr	Thr	Thr	Phe	Leu	Leu	Leu	Phe	Gln	Tyr	Cys	210	215	220	
Leu	Pro	Leu	Gly	Phe	Ile	Leu	Val	Cys	Tyr	Ala	Arg	Ile	Tyr	Arg	Arg	225	230	235	240
Leu	Gln	Arg	Gln	Gly	Arg	Val	Phe	His	Lys	Gly	Thr	Tyr	Ser	Leu	Arg	245	250	255	
Ala	Gly	His	Met	Lys	Gln	Val	Asn	Val	Val	Leu	Val	Val	Met	Val	Val	260	265	270	
Ala	Phe	Ala	Val	Leu	Trp	Leu	Pro	Leu	His	Val	Phe	Asn	Ser	Leu	Glu	275	280	285	
Asp	Trp	His	His	Glu	Ala	Ile	Pro	Ile	Cys	His	Gly	Asn	Leu	Ile	Phe	290	295	300	
Leu	Val	Cys	His	Leu	Leu	Ala	Met	Ala	Ser	Thr	Cys	Val	Asn	Pro	Phe	305	310	315	320
Ile	Tyr	Gly	Phe	Leu	Asn	Thr	Asn	Phe	Lys	Lys	Glu	Ile	Lys	Ala	Leu	325	330	335	
Val	Leu	Thr	Cys	Gln	Gln	Ser	Ala	Pro	Leu	Glu	Glu	Ser	Glu	His	Leu	340	345	350	
Pro	Leu	Ser	Thr	Val	His	Thr	Glu	Val	Ser	Lys	Gly	Ser	Leu	Arg	Leu	355	360	365	
Ser	Gly	Arg	Ser	Asn	Pro	Ile										370	375		

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTGCTTATGG GGCTGTGATT ATTCTTGGGG TCTCTGGAAA CCTGG

45

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TAGGATGATT ATGATCAATG CCAGGTTTCC AGAGACCCCA AGAAT

45

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAAGAGATGA GGAATGTCAC CAACATTCTG ATCGTGAACC TCTCC

45

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAGCAAGTCT GAGAAGGAGA GGTTACGAT CAGAATGTTG GTGAC

45

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGCAAACTGA ATCCTTTTGT GCAATGCGTC TCCATTACAG TATCCATTTT CTCT

54

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACGTTCCACA GCGATGAGAA CCAGAGAGAA AATGGATACT GTAATGGAGA CGCA

54

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTGCAGTATT TTGCCCCACT CTGTTTCATA TTCATATGCT AC

42

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAAGCGAATG TATATCTTGA AGTAGCATAT GAATATGAAA CA

42

(2). INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTGCTCTGCC ACCTCACGGC CATGATCTCC ACCTGCGTCA ACCCCATC

48

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAAATTTTTCG TTCAGGAATC CATAAAAGAT GGGGTTGACG CAGGTGGA

48

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TCATCGTCAC TTCCTACAGC ATTGAGACTG TCGTGGGGGT CCTGGGT

47

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACAGTCACAC ACATCAGGCA GAGGTTACCC AGGACCCCCA CGACAG

46

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGCTTATCGC CAACCTGGCC TTCTCTGACT TCCTCATGTG CCTCC

45

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TAGACGGCGG TCAGCGGCTG GCAGAGGAGG CACATGAGGA AGTCA

45

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TGTCGGCCTT CATCCAGTGC ATGTCGGTGA CGGTCTCCAT CCTCT

45

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTCTCCAGGG CCACGAGGAC GAGCGAGAGG ATGGAGACCG TCACC

45

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCCTACCTGG GGATTGTGCT CATCTGGGTC ATGCCTGTG TCCTC

45

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGCTGTTGGC CAGGAAGGGC AGGGAGAGGA CACAGGCAAT GACCC

45

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CATCTACACC ACCTTCCTGC TCCTCTTCCA GTACTGCCTC CCACT

45

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGCATAACAG ACCAGGATGA AGCCAGTGG GAGGCAGTAC TGGAA

45

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTGGTGGTGA TGGTGGTGGC CTTTGCCGTG CTCTGGCTGC CTCTGC

46

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CAGTCTTCCA GGCTGTTGAA CACATGCAGA GGCAGCCAGA GCACG

45

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATCTTCTTAG TGTGCCACTT GCTTGCCATG GCCTCCACCT GCGTC

45

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGAGAAAGCC ATAGATGAAT GGGTTGACGC AGGTGGAGGC CATGG

45

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 178..1306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATAGCTCTCA AGCCATAAGA TATAAGTAGC TAAGAATTGT CTCCCTCTCC CTGTCCCTTG	60
TTCTTACCTG GTTCCATTTT ACATGCCTGG ACCTTTGAGT TCCATTTGTT TGTTTTGCAG	120
GCTACACTCA GAAGTGGGCC CTTTAGTCTT GAAGTTCCTG GTCTTCTCAC ACCCACC	177
ATG AAT ACC TCT CAT CTC ATG GCC TCC CTT TCT CCG GCA TTC CTA CAA	225
Met Asn Thr Ser His Leu Met Ala Ser Leu Ser Pro Ala Phe Leu Gln	
1 5 10 15	
GGT AAG AAT GGG ACC AAC CCA CTG GAT TCC CTC TAT AAT CTC TCT GAC	273
Gly Lys Asn Gly Thr Asn Pro Leu Asp Ser Leu Tyr Asn Leu Ser Asp	
20 25 30	
GGC TGC CAG GAT TCG GCA GAT CTG TTG GCC TTC ATC ATC ACC ACC TAC	321
Gly Cys Gln Asp Ser Ala Asp Leu Leu Ala Phe Ile Ile Thr Thr Tyr	
35 40 45	
AGC GTT GAG ACC GTC TTG GGG GTC CTA GGA AAC CTC TGC TTG ATA TTT	369
Ser Val Glu Thr Val Leu Gly Val Leu Gly Asn Leu Cys Leu Ile Phe	
50 55 60	
GTG ACC ACA AGG CAA AAG GAA AAG TCC AAT GTG ACC AAC CTA CTC ATT	417
Val Thr Thr Arg Gln Lys Glu Lys Ser Asn Val Thr Asn Leu Leu Ile	
65 70 75 80	
GCC AAC CTG GCC TTC TCT GAC TTC CTC ATG TGT CTC ATC TGC CAG CCG	465
Ala Asn Leu Ala Phe Ser Asp Phe Leu Met Cys Leu Ile Cys Gln Pro	
85 90 95	
CTC ACG GTC ACC TAC ACC ATC ATG GAC TAC TGG ATC TTC GGC GAA GTC	513
Leu Thr Val Thr Tyr Thr Ile Met Asp Tyr Trp Ile Phe Gly Glu Val	
100 105 110	

CTT TGC AAG ATG TTA ACG TTC ATC CAG TGT ATG TCG GTG ACA GTC TCC	561
Leu Cys Lys Met Leu Thr Phe Ile Gln Cys Met Ser Val Thr Val Ser	
115 120 125	
ATC CTC TCA CTG GTC CTT GTG GCC CTG GAG AGG CAC CAG CTC ATT ATC	609
Ile Leu Ser Leu Val Leu Val Ala Leu Glu Arg His Gln Leu Ile Ile	
130 135 140	
AAC CCG ACT GGC TGG AAA CCC AGC ATT TCC CAG GCC TAC CTG GGG ATT	657
Asn Pro Thr Gly Trp Lys Pro Ser Ile Ser Gln Ala Tyr Leu Gly Ile	
145 150 155 160	
GTG GTC ATC TGG TTC ATT TCT TGT TTC CTC TCC TTG CCC TTC CTG GCC	705
Val Val Ile Trp Phe Ile Ser Cys Phe Leu Ser Leu Pro Phe Leu Ala	
165 170 175	
AAT AGC ATC CTG AAC GAC CTC TTC CAC TAC AAC CAC TCT AAG GTT GTG	753
Asn Ser Ile Leu Asn Asp Leu Phe His Tyr Asn His Ser Lys Val Val	
180 185 190	
GAG TTT CTG GAA GAC AAG GTT GTC TGC TTT GTG TCC TGG TCC TCG GAT	801
Glu Phe Leu Glu Asp Lys Val Val Cys Phe Val Ser Trp Ser Ser Asp	
195 200 205	
CAC CAC CGC CTC ATC TAC ACC ACC TTT CTG CTG CTC TTC CAA TAC TGC	849
His His Arg Leu Ile Tyr Thr Thr Phe Leu Leu Leu Phe Gln Tyr Cys	
210 215 220	
GTC CCT CTG GCC TTC ATC CTG GTC TGC TAC ATG CGT ATC TAT CAG CGC	897
Val Pro Leu Ala Phe Ile Leu Val Cys Tyr Met Arg Ile Tyr Gln Arg	
225 230 235 240	
CTG CAG AGG CAG AGG CGT GCG TTC CAC ACG CAC ACT TGC AGC TCA CGA	945
Leu Gln Arg Gln Arg Arg Ala Phe His Thr His Thr Cys Ser Ser Arg	
245 250 255	
GTG GGG CAG ATG AAG CGG ATC AAT GGC ATG CTC ATG GCA ATG GTG ACT	993
Val Gly Gln Met Lys Pro Ile Asn Gly Met Leu Met Ala Met Val Thr	
260 265 270	
GCC TTT GCA GTT CTC TGG CTG CCC CTG CAT GTG TTC AAC ACT CTG GAG	1041
Ala Phe Ala Val Leu Trp Leu Pro Leu His Val Phe Asn Thr Leu Glu	
275 280 285	
GAC TGG TAC CAG GAA GCC ATC CCT GCT TGC CAT GGC AAC CTC ATC TTC	1089
Asp Trp Tyr Gln Glu Ala Ile Pro Ala Cys His Gly Asn Leu Ile Phe	
290 295 300	
TTG ATG TGC CAC CTG TTT GCC ATG GCT TCC ACC TGT GTC AAC CCT TTC	1137
Leu Met Cys His Leu Phe Ala Met Ala Ser Thr Cys Val Asn Pro Phe	
305 310 315 320	
ATC TAT GGC TTT CTC AAC ATC AAC TTC AAG AAG GAC ATC AAG GCT CTG	1185
Ile Tyr Gly Phe Leu Asn Ile Asn Phe Lys Lys Asp Ile Lys Ala Leu	
325 330 335	
GTT CTG ACC TGC CGT TGC AGG CCA CCT CAA GGG GAG CCT GAG CCT CTG	1233
Val Leu Thr Cys Arg Cys Arg Pro Pro Gln Gly Glu Pro Glu Pro Leu	
340 345 350	
CCC CTG TCC ACT GTG CAC ACG GAC CTC TCC AAG GGA TCT ATG AGG ATG	1281
Pro Leu Ser Thr Val His Thr Asp Leu Ser Lys Gly Ser Met Arg Met	
355 360 365	

GGT AGC AAG TCT AAC GTC ATG TAG T CATGTCTAGG CTCTTCCGCC 1326
 Gly Ser Lys Ser Asn Val Met *
 370 375

ATTTCTTTTCG ACACACCCTT TCACTGAGCT AAGTAGACAC AATGCAAGCT GTGGTATCAT 1386

CCTGCCATTT CTGGTCTTTG GGGCCCAGAC AGGCGGCAAG AGACTTGAAG CTT 1439

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Asn	Thr	Ser	His	Leu	Met	Ala	Ser	Leu	Ser	Pro	Ala	Phe	Leu	Gln
1				5					10					15	
Gly	Lys	Asn	Gly	Thr	Asn	Pro	Leu	Asp	Ser	Leu	Tyr	Asn	Leu	Ser	Asp
		20						25					30		
Gly	Cys	Gln	Asp	Ser	Ala	Asp	Leu	Leu	Ala	Phe	Ile	Ile	Thr	Thr	Tyr
		35					40					45			
Ser	Val	Glu	Thr	Val	Leu	Gly	Val	Leu	Gly	Asn	Leu	Cys	Leu	Ile	Phe
	50					55					60				
Val	Thr	Thr	Arg	Gln	Lys	Glu	Lys	Ser	Asn	Val	Thr	Asn	Leu	Leu	Ile
	65			70					75					80	
Ala	Asn	Leu	Ala	Phe	Ser	Asp	Phe	Leu	Met	Cys	Leu	Ile	Cys	Gln	Pro
			85						90					95	
Leu	Thr	Val	Thr	Tyr	Thr	Ile	Met	Asp	Tyr	Trp	Ile	Phe	Gly	Glu	Val
		100						105					110		
Leu	Cys	Lys	Met	Leu	Thr	Phe	Ile	Gln	Cys	Met	Ser	Val	Thr	Val	Ser
		115					120					125			
Ile	Leu	Ser	Leu	Val	Leu	Val	Ala	Leu	Glu	Arg	His	Gln	Leu	Ile	Ile
	130					135					140				
Asn	Pro	Thr	Gly	Trp	Lys	Pro	Ser	Ile	Ser	Gln	Ala	Tyr	Leu	Gly	Ile
	145				150					155				160	
Val	Val	Ile	Trp	Phe	Ile	Ser	Cys	Phe	Leu	Ser	Leu	Pro	Phe	Leu	Ala
			165						170					175	
Asn	Ser	Ile	Leu	Asn	Asp	Leu	Phe	His	Tyr	Asn	His	Ser	Lys	Val	Val
		180						185					190		
Glu	Phe	Leu	Glu	Asp	Lys	Val	Val	Cys	Phe	Val	Ser	Trp	Ser	Ser	Asp
		195					200					205			
His	His	Arg	Leu	Ile	Tyr	Thr	Thr	Phe	Leu	Leu	Leu	Phe	Gln	Tyr	Cys
	210					215					220				
Val	Pro	Leu	Ala	Phe	Ile	Leu	Val	Cys	Tyr	Met	Arg	Ile	Tyr	Gln	Arg

225		230		235		240									
Leu	Gln	Arg	Gln	Arg	Arg	Ala	Phe	His	Thr	His	Thr	Cys	Ser	Ser	Arg
			245						250					255	
Val	Gly	Gln	Met	Lys	Pro	Ile	Asn	Gly	Met	Leu	Met	Ala	Met	Val	Thr
			260					265					270		
Ala	Phe	Ala	Val	Leu	Trp	Leu	Pro	Leu	His	Val	Phe	Asn	Thr	Leu	Glu
		275					280					285			
Asp	Trp	Tyr	Gln	Glu	Ala	Ile	Pro	Ala	Cys	His	Gly	Asn	Leu	Ile	Phe
	290					295					300				
Leu	Met	Cys	His	Leu	Phe	Ala	Met	Ala	Ser	Thr	Cys	Val	Asn	Pro	Phe
305					310					315					320
Ile	Tyr	Gly	Phe	Leu	Asn	Ile	Asn	Phe	Lys	Lys	Asp	Ile	Lys	Ala	Leu
				325					330					335	
Val	Leu	Thr	Cys	Arg	Cys	Arg	Pro	Pro	Gln	Gly	Glu	Pro	Glu	Pro	Leu
			340					345					350		
Pro	Leu	Ser	Thr	Val	His	Thr	Asp	Leu	Ser	Lys	Gly	Ser	Met	Arg	Met
		355					360					365			
Gly	Ser	Lys	Ser	Asn	Val	Met	*								
	370					375									

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CGCGTGTTTC ACAAGGGCAC CTA

23

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGCCACTTAG CCTCAGGGAC CC

22

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TCCGTATGTA CTGTGGACAG GGCAGATGC TCCGACTCCT CCAGG

45

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 350 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met	Asn	Thr	Ser	His	Leu	Met	Ala	Ser	Leu	Ser	Pro	Ala	Phe	Leu	Gln
1				5					10					15	
Gly	Lys	Asn	Gly	Thr	Asn	Pro	Leu	Asp	Ser	Leu	Tyr	Asn	Leu	Ser	Asp
			20					25					30		
Gly	Cys	Gln	Asp	Ser	Ala	Asp	Leu	Leu	Ala	Phe	Ile	Ile	Thr	Thr	Tyr
		35					40					45			
Ser	Val	Glu	Thr	Val	Leu	Gly	Val	Leu	Gly	Asn	Leu	Cys	Leu	Ile	Phe
		50				55					60				
Val	Thr	Thr	Arg	Gln	Lys	Glu	Lys	Ser	Asn	Val	Thr	Asn	Leu	Leu	Ile
65				70					75					80	
Ala	Asn	Leu	Ala	Phe	Ser	Asp	Phe	Leu	Met	Cys	Leu	Ile	Cys	Gln	Pro
			85						90				95		
Leu	Thr	Val	Thr	Tyr	Thr	Ile	Met	Asp	Tyr	Trp	Ile	Phe	Gly	Glu	Val
			100					105					110		
Leu	Cys	Lys	Met	Leu	Thr	Phe	Ile	Gln	Cys	Met	Ser	Val	Thr	Val	Ser
			115					120				125			
Ile	Leu	Ser	Leu	Val	Leu	Val	Ala	Leu	Glu	Arg	His	Gln	Leu	Ile	Ile
			130			135					140				
Asn	Pro	Thr	Gly	Trp	Lys	Pro	Ser	Ile	Ser	Gln	Ala	Tyr	Leu	Gly	Ile
145					150					155					160

Val Val Ile Trp Phe Ile Ser Cys Phe Leu Ser Leu Pro Phe Leu Ala
 165 170 175
 Asn Ser Ile Leu Asn Asp Leu Phe His Tyr Asn His Ser Lys Val Val
 180 185 190
 Glu Phe Leu Glu Asp Lys Val Val Cys Phe Val Ser Trp Ser Ser Asp
 195 200 205
 His His Arg Leu Ile Tyr Thr Thr Phe Leu Leu Leu Phe Gln Tyr Cys
 210 215 220
 Val Pro Leu Ala Phe Ile Leu Val Cys Tyr Met Arg Ile Tyr Gln Arg
 225 230 235 240
 Leu Gln Arg Gln Arg Arg Ala Phe His Thr His Thr Cys Ser Ser Arg
 245 250 255
 Val Gly Gln Met Lys Arg Ile Asn Gly Met Leu Met Ala Met Val Thr
 260 265 270
 Ala Phe Ala Val Leu Trp Leu Pro Leu His Val Phe Asn Thr Leu Glu
 275 280 285
 Asp Trp Tyr Gln Glu Ala Ile Pro Ala Cys His Gly Asn Leu Ile Phe
 290 295 300
 Leu Met Cys His Leu Phe Ala Met Ala Ser Thr Cys Val Asn Pro Phe
 305 310 315 320
 Ile Tyr Gly Phe Leu Asn Ile Asn Phe Lys Lys Asp Ile Lys Ala Leu
 325 330 335
 Val Leu Thr Cys Arg Cys Arg Pro Pro Gln Gly Glu Pro Glu
 340 345 350

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 350 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Asn Thr Ser His Leu Leu Ala Leu Leu Leu Pro Lys Ser Pro Gln
 1 5 10 15
 Gly Glu Asn Arg Ser Lys Pro Leu Gly Thr Pro Tyr Asn Phe Ser Glu
 20 25 30
 His Cys Gln Asp Ser Val Asp Val Met Val Phe Ile Val Thr Ser Tyr
 35 40 45
 Ser Ile Glu Thr Val Val Gly Val Leu Gly Asn Leu Cys Leu Met Cys
 50 55 60
 Val Thr Val Arg Gln Lys Glu Lys Ala Asn Val Thr Asn Leu Leu Ile
 65 70 75 80

Ala Asn Leu Ala Phe Ser Asp Phe Leu Met Cys Leu Leu Cys Gln Pro
 85 90 95
 Leu Thr Ala Val Tyr Thr Ile Met Asp Tyr Trp Ile Phe Gly Glu Thr
 100 105 110
 Leu Cys Lys Met Ser Ala Phe Ile Gln Cys Met Ser Val Thr Val Ser
 115 120 125
 Ile Leu Ser Leu Val Leu Val Ala Leu Glu Arg His Gln Leu Ile Ile
 130 135 140
 Asn Pro Thr Gly Trp Lys Pro Ser Ile Ser Gln Ala Tyr Leu Gly Ile
 145 150 155 160
 Val Leu Ile Trp Val Ile Ala Cys Val Leu Ser Leu Pro Phe Leu Ala
 165 170 175
 Asn Ser Ile Leu Glu Asn Val Phe His Lys Asn His Ser Lys Ala Leu
 180 185 190
 Glu Phe Leu Ala Asp Lys Val Val Cys Thr Glu Ser Trp Pro Leu Ala
 195 200 205
 His His Arg Thr Ile Tyr Thr Thr Phe Leu Leu Leu Phe Gln Tyr Cys
 210 215 220
 Leu Pro Leu Gly Phe Ile Leu Val Cys Tyr Ala Arg Ile Tyr Arg Arg
 225 230 235 240
 Leu Gln Arg Gln Gly Arg Val Phe His Lys Gly Thr Tyr Ser Leu Arg
 245 250 255
 Ala Gly His Met Lys Gln Val Asn Val Val Leu Val Val Met Val Val
 260 265 270
 Ala Phe Ala Val Leu Trp Leu Pro Leu His Val Phe Asn Ser Leu Glu
 275 280 285
 Asp Trp His His Glu Ala Ile Pro Ile Cys His Gly Asn Leu Ile Phe
 290 295 300
 Leu Val Cys His Leu Leu Ala Met Ala Ser Thr Cys Val Asn Pro Phe
 305 310 315 320
 Ile Tyr Gly Phe Leu Asn Thr Asn Phe Lys Lys Glu Ile Lys Ala Leu
 325 330 335
 Val Leu Thr Cys Gln Gln Ser Ala Pro Leu Glu Glu Ser Glu
 340 345 350

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met	Asn	Ser	Thr	Leu	Phe	Ser	Gln	Val	Glu	Asn	His	Ser	Val	His	Ser		
1				5					10					15			
Asn	Phe	Ser	Glu	Lys	Asn	Ala	Gln	Leu	Leu	Ala	Phe	Glu	Asn	Asp	Asp		
			20					25					30				
Cys	His	Leu	Pro	Leu	Ala	Met	Ile	Phe	Thr	Leu	Ala	Leu	Ala	Tyr	Gly		
		35					40					45					
Ala	Val	Ile	Ile	Leu	Gly	Val	Ser	Gly	Asn	Leu	Ala	Leu	Ile	Ile	Ile		
	50					55					60						
Ile	Leu	Lys	Gln	Lys	Glu	Met	Arg	Asn	Val	Thr	Asn	Ile	Leu	Ile	Val		
65				70						75					80		
Asn	Leu	Ser	Phe	Ser	Asp	Leu	Leu	Val	Ala	Ile	Met	Cys	Leu	Pro	Phe		
				85					90					95			
Thr	Phe	Val	Tyr	Thr	Leu	Met	Asp	His	Trp	Val	Phe	Gly	Glu	Ala	Met		
			100					105					110				
Cys	Lys	Leu	Asn	Pro	Phe	Val	Gln	Cys	Val	Ser	Ile	Thr	Val	Ser	Ile		
		115					120					125					
Phe	Ser	Leu	Val	Leu	Ile	Ala	Val	Glu	Arg	His	Gln	Leu	Ile	Ile	Asn		
	130					135					140						
Pro	Arg	Gly	Trp	Arg	Pro	Asn	Asn	Arg	His	Ala	Tyr	Val	Gly	Ile	Ala		
145					150					155					160		
Val	Ile	Trp	Val	Leu	Ala	Val	Ala	Ser	Ser	Leu	Pro	Phe	Leu	Ile	Tyr		
				165					170					175			
Gln	Val	Met	Thr	Asp	Glu	Pro	Phe	Gln	Asn	Val	Thr	Leu	Asp	Ala	Tyr		
			180					185					190				
Lys	Asp	Lys	Tyr	Val	Cys	Phe	Asp	Gln	Phe	Pro	Ser	Asp	Ser	His	Arg		
	195						200					205					
Leu	Ser	Tyr	Thr	Thr	Leu	Leu	Leu	Val	Leu	Gln	Tyr	Phe	Gly	Pro	Leu		
	210				215						220						
Cys	Phe	Ile	Phe	Ile	Cys	Tyr	Phe	Lys	Ile	Tyr	Ile	Arg	Leu	Lys	Arg		
225					230					235					240		
Arg	Asn	Asn	Met	Met	Asp	Lys	Met	Arg	Asp	Asn	Lys	Tyr	Arg	Ser	Ser		
			245						250					255			
Glu	Thr	Lys	Arg	Ile	Asn	Ile	Met	Leu	Leu	Ser	Ile	Val	Val	Ala	Phe		
			260					265					270				
Ala	Val	Cys	Trp	Leu	Pro	Leu	Thr	Ile	Phe	Asn	Thr	Val	Phe	Asp	Trp		
		275					280					285					
Asn	His	Gln	Ile	Ile	Ala	Thr	Cys	Asn	His	Asn	Leu	Leu	Phe	Leu	Leu		
	290					295					300						
Cys	His	Leu	Thr	Ala	Met	Ile	Ser	Thr	Cys	Val	Asn	Pro	Ile	Phe	Tyr		
305					310					315					320		

(2) INFORMATION FOR SEQ ID NO:35:

(ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: NO

Met 1	Asn	Ser	Thr	Leu 5	Phe	Ser	Arg	Val	Glu 10	Asn	Tyr	Ser	Val	His 15	Tyr
Asn	Val	Ser	Glu 20	Asn	Ser	Pro	Phe	Leu 25	Ala	Phe	Glu	Asn	Asp 30	Asp	Cys
His	Leu	Pro 35	Leu	Ala	Val	Ile	Phe 40	Thr	Leu	Ala	Leu	Ala 45	Tyr	Gly	Ala
Val	Ile 50	Ile	Leu	Gly	Val	Ser 55	Gly	Asn	Leu	Ala	Leu 60	Ile	Ile	Ile	Ile
Leu 65	Lys	Gln	Lys	Glu	Met 70	Arg	Asn	Val	Thr	Asn 75	Ile	Leu	Ile	Val	Asn 80
Leu	Ser	Phe	Ser	Asp 85	Leu	Leu	Val	Ala	Val 90	Met	Cys	Leu	Pro	Phe 95	Thr
Phe	Val	Tyr	Thr 100	Leu	Met	Asp	His	Trp 105	Val	Phe	Gly	Glu	Thr 110	Met	Cys
Lys	Leu	Asn 115	Pro	Phe	Val	Gln	Cys 120	Val	Ser	Ile	Thr	Val 125	Ser	Ile	Phe
Ser	Leu 130	Val	Leu	Ile	Ala	Val 135	Glu	Arg	His	Gln	Leu 140	Ile	Ile	Asn	Pro
Arg 145	Gly	Trp	Arg	Pro	Asn 150	Asn	Arg	His	Ala	Tyr 155	Ile	Gly	Ile	Thr	Val 160
Ile	Trp	Val	Leu	Ala 165	Val	Ala	Ser	Ser	Leu 170	Pro	Phe	Val	Ile	Tyr 175	Gln
Ile	Leu	Thr	Asp	Glu	Pro	Phe	Gln	Asn	Val	Ser	Leu	Ala	Ala	Phe	Lys

180	185	190
Asp Lys Tyr Val Cys Phe Asp	Lys Phe Pro Ser Asp	Ser His Arg Leu
195	200	205
Ser Tyr Thr Thr Leu Leu Leu	Val Leu Gln Tyr Phe Gly	Pro Leu Cys
210	215	220
Phe Ile Phe Ile Cys Tyr Phe	Lys Ile Tyr Ile Arg Leu	Lys Arg Arg
225	230	235
Asn Asn Met Met Asp Lys Ile	Arg Asp Ser Lys Tyr Arg	Ser Ser Glu
245	250	255
Thr Lys Arg Ile Asn Val Met	Leu Leu Ser Ile Val Val	Ala Phe Ala
260	265	270
Val Cys Trp Leu Pro Leu Thr	Ile Phe Asn Thr Val Phe	Asp Trp Asn
275	280	285
His Gln Ile Ile Ala Thr Cys	Asn His Asn Leu Leu Phe	Leu Leu Cys
290	295	300
His Leu Thr Ala Met Ile Ser	Thr Cys Val Asn Pro Ile	Phe Tyr Gly
305	310	315
Phe Leu Asn Lys Asn Phe Gln	Arg Asp Leu Gln Phe Phe	Phe Asn Phe
325	330	335
Cys Asp Phe Arg Ser Arg Asp	Asp Asp Tyr Glu Thr Ile	Ala Met Ser
340	345	350
Thr Met His Thr Asp Val Ser	Lys Thr Ser Leu Lys Gln	Ala Ser Pro
355	360	365
Val Ala Phe Lys Lys Ile Ser	Met Asn Asp Asn Glu Lys	Ile
370	375	380

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Asn Ser Thr Leu Phe Ser Lys Val	Glu Asn His Ser Ile His Tyr
1	15
Asn Ala Ser Glu Asn Ser Pro Leu Leu Ala	Phe Glu Asn Asp Asp Cys
20	30
His Leu Pro Leu Ala Val Ile Phe Thr	Leu Ala Leu Ala Tyr Gly Ala
35	45

Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile Ile
 50 55 60
 Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val Asn
 65 70 75 80
 Leu Ser Phe Ser Asp Leu Leu Val Ala Val Met Cys Leu Pro Phe Thr
 85 90 95
 Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Thr Met Cys
 100 105 110
 Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile Phe
 115 120 125
 Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn Pro
 130 135 140
 Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Ile Gly Ile Thr Val
 145 150 155 160
 Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Val Ile Tyr Gln
 165 170 175
 Ile Leu Thr Asp Glu Pro Phe Gln Asn Val Ser Leu Ala Ala Phe Lys
 180 185 190
 Asp Lys Tyr Val Cys Phe Asp Lys Phe Pro Ser Asp Ser His Arg Leu
 195 200 205
 Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu Cys
 210 215 220
 Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg Arg
 225 230 235 240
 Asn Asn Met Met Asp Lys Ile Arg Asp Ser Lys Tyr Arg Ser Ser Glu
 245 250 255
 Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val Ala Phe Ala
 260 265 270
 Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp Asn
 275 280 285
 His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu Cys
 290 295 300
 His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr Gly
 305 310 315 320
 Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Phe Asn Phe
 325 330 335
 Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met Ser
 340 345 350
 Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro
 355 360 365
 Val Ala Phe Lys Lys Ile Ser Met Asn Asp Asn Glu Lys Val
 370 375 380